

SEQUENCE LISTING

<110> Farese, Robert V.
Cases, Sylvaine
Smith, Steven
Erickson, Sandra

<120> Diacylglycerol O-Acyltransferase

<130> 6510-105CIP2

<150> 60/107,771

<151> 1998-11-09

<150> PCT/US98/17883

<151> 1998-08-28

<150> 09/103,754

<151> 1998-06-24

<150> 09/339,472

<151> 1999-06-23

<160> 10

<170> FastSEQ for Windows Version 3.0

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<212> DNA

<213> homo sapiens

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 gggtgacact catcattggg caaccgggtg ctgtgctcat gtatgtccac gactactacg 1560
 tgctcaacta cgatgccccg gtgggggtat gagctactgc caaaggccag ccctccctaa 1620
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<220>
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 attcatggga ttataatag aacaatatat aaatcctatt gtcaggaact caaagcatcc 120

tttgaaaggc	gatcttctat	atgctattga	aagagtgttg	aagctttcag	ttccaaattt	180
atatgtgtgg	ctctgcatgt	tctactgctt	cttccacctt	tggttaaaca	tattggcaga	240
gcttctctgc	ttcggggatc	gtgaattcta	caaagattgg	tggaatgcaa	aaagtgtggg	300
agattactgg	gagaatgtgg	aatatgcttg	tccataaatg	ggatgggtcc	gacatatata	360
ccttccccgt	gcttgcgcac	aaggattacc	caaagacacc	ccggccatta	accattggct	420
ttcccaagcc	ccctggaggg	ctttccatgg	gccanggacc	cgngtncctt	tggcngggcc	480
ttcaaagcaa	agggggnttn	cctggggnta	aagntccang	ggcccttggg	gcccanccaa	540
aannttcccc	cgggaaaggg	ttgcccaccg	gggggngaaa	aanncccggg	ggcaccncgg	600
aattttggga	acccgggggg	ggcctttttt				629

<210> 5
 <211> 386
 <212> PRT
 <213> homo sapiens

<400> 5

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Cys	Leu	Val	Ile	Ala	Ala	Asn	Val	Phe	Ala	Val	Ala	Ala	Phe	Gln	Val	35	40	45	
Glu	Lys	Arg	Leu	Ala	Val	Gly	Ala	Leu	Thr	Glu	Gln	Ala	Gly	Leu	Leu	50	55	60	
Leu	His	Val	Ala	Asn	Leu	Ala	Thr	Ile	Leu	Cys	Phe	Pro	Ala	Ala	Val	65	70	75	80
Val	Leu	Leu	Val	Glu	Ser	Ile	Thr	Pro	Val	Gly	Ser	Leu	Leu	Ala	Leu	85	90	95	
Met	Ala	His	Thr	Ile	Leu	Phe	Leu	Lys	Leu	Phe	Ser	Tyr	Arg	Asp	Val	100	105	110	
Asn	Ser	Trp	Cys	Arg	Arg	Ala	Arg	Ala	Lys	Ala	Ala	Ser	Ala	Gly	Lys	115	120	125	
Lys	Ala	Ser	Ser	Val	Ala	Ala	Pro	His	Thr	Val	Ser	Tyr	Pro	Asp	Asn	130	135	140	
Leu	Thr	Tyr	Arg	Asp	Leu	Tyr	Tyr	Phe	Leu	Phe	Ala	Pro	Thr	Leu	Cys	145	150	155	160
Tyr	Glu	Leu	Asn	Phe	Pro	Arg	Ser	Pro	Arg	Ile	Arg	Lys	Arg	Phe	Leu	165	170	175	
Leu	Arg	Arg	Ile	Leu	Glu	Met	Leu	Phe	Phe	Thr	Gln	Leu	Gln	Val	Gly	180	185	190	
Leu	Ile	Gln	Gln	Trp	Met	Val	Pro	Thr	Ile	Gln	Asn	Ser	Met	Lys	Pro	195	200	205	
Phe	Lys	Asp	Met	Asp	Tyr	Ser	Arg	Ile	Ile	Glu	Arg	Leu	Leu	Lys	Leu	210	215	220	
Ala	Val	Pro	Asn	His	Leu	Ile	Trp	Leu	Ile	Phe	Phe	Tyr	Trp	Leu	Phe	225	230	235	240
His	Ser	Cys	Leu	Asn	Ala	Val	Ala	Glu	Leu	Met	Gln	Phe	Gly	Asp	Arg	245	250	255	
Glu	Phe	Tyr	Arg	Asp	Trp	Trp	Asn	Ser	Glu	Ser	Val	Thr	Tyr	Phe	Trp	260	265	270	
Gln	Asn	Trp	Asn	Ile	Pro	Val	His	Lys	Trp	Cys	Ile	Arg	His	Phe	Tyr	275	280	285	
Lys	Pro	Met	Leu	Arg	Arg	Gly	Ser	Ser	Lys	Trp	Met	Ala	Arg	Thr	Gly	290	295	300	
Val	Phe	Leu	Ala	Ser	Ala	Phe	Phe	His	Glu	Tyr	Leu	Val	Ser	Val	Pro	305	310	315	320
Leu	Arg	Met	Phe	Arg	Leu	Trp	Ala	Phe	Thr	Gly	Met	Met	Ala	Gln	Ile	325	330	335	
Pro	Leu	Ala	Trp	Phe	Val	Gly	Arg	Phe	Gln	Gly	Asn	Tyr	Gly	Asn		340	345	350	
Ala	Ala	Val	Trp	Leu	Ser	Leu	Ile	Ile	Gly	Gln	Pro	Ile	Ala	Val	Leu				

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 Glu Ala
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 <213> homo sapiens

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 Asp Ala Ala Ala Gly Pro Asp Val Gly Ala Ala Gly Asp Ala Pro Ala
 35 40 45
 Pro Ala Pro Asn Lys Asp Gly Asp Ala Gly Val Gly Ser Gly His Trp
 50 55 60
 Glu Leu Arg Cys His Arg Leu Gln Asp Ser Leu Phe Ser Ser Asp Ser
 65 70 75 80
 Gly Phe Ser Asn Tyr Arg Gly Ile Leu Asn Trp Cys Val Val Met Leu
 85 90 95
 Ile Leu Ser Asn Ala Arg Leu Phe Leu Glu Asn Leu Ile Lys Tyr Gly
 100 105 110
 Ile Leu Val Asp Pro Ile Gln Val Val Ser Leu Phe Leu Lys Asp Pro
 115 120 125
 His Ser Trp Pro Ala Pro Cys Leu Val Ile Ala Ala Asn Val Phe Ala
 130 135 140
 Val Ala Ala Phe Gln Val Glu Lys Arg Leu Ala Val Gly Ala Leu Thr
 145 150 155 160
 Glu Gln Ala Gly Leu Leu Leu His Val Ala Asn Leu Ala Thr Ile Leu
 165 170 175
 Cys Phe Pro Ala Ala Val Val Leu Leu Val Glu Ser Ile Thr Pro Val
 180 185 190
 Gly Ser Leu Leu Ala Leu Met Ala His Thr Ile Leu Phe Leu Lys Leu
 195 200 205
 Phe Ser Tyr Arg Asp Val Asn Ser Trp Cys Arg Arg Ala Arg Ala Lys
 210 215 220
 Ala Ala Ser Ala Gly Lys Lys Ala Ser Ser Ala Ala Ala Pro His Thr
 225 230 235 240
 Val Ser Tyr Pro Asp Asn Leu Thr Tyr Arg Asp Leu Tyr Tyr Phe Leu
 245 250 255
 Phe Ala Pro Thr Leu Cys Tyr Glu Leu Asn Phe Pro Arg Ser Pro Arg
 260 265 270
 Ile Arg Lys Arg Phe Leu Leu Arg Arg Ile Leu Glu Met Leu Phe Phe
 275 280 285
 Thr Gln Leu Gln Val Gly Leu Ile Gln Gln Trp Met Val Pro Thr Ile
 290 295 300
 Gln Asn Ser Met Lys Pro Phe Lys Asp Met Asp Tyr Ser Arg Ile Ile
 305 310 315 320
 Glu Arg Leu Leu Lys Leu Ala Val Pro Asn His Leu Ile Trp Leu Ile
 325 330 335
 Phe Phe Tyr Trp Leu Phe His Ser Cys Leu Asn Ala Val Ala Glu Leu
 340 345 350
 Met Gln Phe Gly Asp Arg Glu Phe Tyr Arg Asp Trp Trp Asn Ser Glu
 355 360 365
 Ser Val Thr Tyr Phe Trp Gln Asn Trp Asn Ile Pro Val His Lys Trp
 370 375 380
 Cys Ile Arg His Phe Tyr Lys Pro Met Leu Arg Arg Gly Ser Ser Lys

10040315-102901

385 390 395 400
 Trp Met Ala Arg Thr Gly Val Phe Leu Ala Ser Ala Phe Phe His Glu
 405 410 415
 Tyr Leu Val Ser Val Pro Leu Arg Met Phe Arg Leu Trp Ala Phe Thr
 420 425 430
 Gly Met Met Ala Gln Ile Pro Leu Ala Trp Phe Val Gly Arg Phe Phe
 435 440 445
 Gln Gly Asn Tyr Gly Asn Ala Ala Val Trp Leu Ser Leu Ile Ile Gly
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 465 470 475 480
 Tyr Glu Ala Pro Ala Ala Glu Ala
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 <211> 498
 <212> PRT
 <213> mus musculus

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 35 40 45
 Ala Pro Ala Pro Ala Pro Ala Pro Ala His Thr Arg Asp Lys Asp Gly
 50 55 60
 Arg Thr Ser Val Gly Asp Gly Tyr Trp Asp Leu Arg Cys His Arg Leu
 65 70 75 80
 Gln Asp Ser Leu Phe Ser Ser Asp Ser Gly Phe Ser Asn Tyr Arg Gly
 85 90 95
 Ile Leu Asn Trp Cys Val Val Met Leu Ile Leu Ser Asn Ala Arg Leu
 100 105 110
 Phe Leu Glu Asn Leu Ile Lys Tyr Gly Ile Leu Val Asp Pro Ile Gln
 115 120 125
 Val Val Ser Leu Phe Leu Lys Asp Pro Tyr Ser Trp Pro Ala Pro Cys
 130 135 140
 Val Ile Ile Ala Ser Asn Ile Phe Val Val Ala Ala Phe Gln Ile Glu
 145 150 155 160
 Lys Arg Leu Ala Val Gly Ala Leu Thr Glu Gln Met Gly Leu Leu Leu
 165 170 175
 His Val Val Asn Leu Ala Thr Ile Ile Cys Phe Pro Ala Ala Val Ala
 180 185 190
 Leu Leu Val Glu Ser Ile Thr Pro Val Gly Ser Val Phe Ala Leu Ala
 195 200 205
 Ser Tyr Ser Ile Met Phe Leu Lys Leu Tyr Ser Tyr Arg Asp Val Asn
 210 215 220
 Leu Trp Cys Arg Gln Arg Arg Val Lys Ala Lys Ala Val Ser Thr Gly
 225 230 235 240
 Lys Lys Val Ser Gly Ala Ala Ala Gln Gln Ala Val Ser Tyr Pro Asp
 245 250 255
 Asn Leu Thr Tyr Arg Asp Leu Tyr Tyr Phe Ile Phe Ala Pro Thr Leu
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 Cys Tyr Glu Leu Asn Phe Pro Arg Ser Pro Arg Ile Arg Lys Arg Phe
 275 280 285
 Leu Leu Arg Arg Val Leu Glu Met Leu Phe Phe Thr Gln Leu Gln Val
 290 295 300
 Gly Leu Ile Gln Gln Trp Met Val Pro Thr Ile His Asn Ser Met Lys
 305 310 315 320
 Pro Phe Lys Asp Met Asp Tyr Ser Arg Ile Ile Glu Arg Leu Leu Lys

325 330 335
 Leu Ala Val Pro Asn His Leu Ile Trp Leu Ile Phe Phe Tyr Trp Phe
 340 345 350
 Phe His Ser Cys Leu Asn Ala Val Ala Glu Leu Leu Gln Phe Gly Asp
 355 360 365
 Arg Glu Phe Tyr Arg Asp Trp Trp Asn Ala Glu Ser Val Thr Tyr Phe
 370 375 380
 Trp Gln Asn Trp Asn Ile Pro Val His Lys Trp Cys Ile Arg His Phe
 385 390 395 400
 Tyr Lys Pro Met Leu Arg His Gly Ser Ser Lys Trp Val Ala Arg Thr
 405 410 415
 Gly Val Phe Leu Thr Ser Ala Phe Phe His Glu Tyr Leu Val Ser Val
 420 425 430
 Pro Leu Arg Met Phe Arg Leu Trp Ala Phe Thr Ala Met Met Ala Gln
 435 440 445
 Val Pro Leu Ala Trp Ile Val Gly Arg Phe Phe Gln Gly Asn Tyr Gly
 450 455 460
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 Gly Val

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 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> synthetic peptide-FLAG epitope

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 <213> mus musculus

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atataccccgt	gcacaagtgg	tgcatcagac	acttctacaa	gcctatgctc	agacatggca	1320
gcagcaaagt	ggtggccagg	acaggagtat	ttttgacctc	agccttcttc	catgagtacc	1380
tagtgagcgt	ttccctgcgg	atgttccgcc	tctgggcatt	cacagccatg	atggctcagg	1440
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<210> 10
 <211> 498
 <212> PRT
 <213> mus musculus

<400> 10

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Glu	Val	Arg	Asp	Ala	Ala	Val	Ser	Pro	Asp	Leu	Gly	Ala	Gly	Gly	Asp
			35					40					45		
Ala	Pro	Ala	Pro	Ala	Pro	Ala	His	Thr	Arg	Asp	Lys	Asp	Gly		
			50					55					60		
Arg	Thr	Ser	Val	Gly	Asp	Gly	Tyr	Trp	Asp	Leu	Arg	Cys	His	Arg	Leu
					70					75					80
Gln	Asp	Ser	Leu	Phe	Ser	Ser	Asp	Ser	Gly	Phe	Ser	Asn	Tyr	Arg	Gly
					85					90					95
Ile	Leu	Asn	Trp	Cys	Val	Val	Met	Leu	Ile	Leu	Ser	Asn	Ala	Arg	Leu
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Phe	Leu	Glu	Asn	Leu	Ile	Lys	Tyr	Gly	Ile	Leu	Val	Asp	Pro	Ile	Gln
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Val	Val	Ser	Leu	Phe	Leu	Lys	Asp	Pro	Tyr	Ser	Trp	Pro	Ala	Pro	Cys
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Lys	Arg	Leu	Ala	Val	Gly	Ala	Leu	Thr	Glu	Gln	Met	Gly	Leu	Leu	Leu
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His	Val	Val	Asn	Leu	Ala	Thr	Ile	Ile	Cys	Phe	Pro	Ala	Ala	Val	Ala
					180					185					190
Leu	Leu	Val	Glu	Ser	Ile	Thr	Pro	Val	Gly	Ser	Val	Phe	Ala	Leu	Ala
					195					200					205
Ser	Tyr	Ser	Ile	Met	Phe	Leu	Lys	Leu	Tyr	Ser	Tyr	Arg	Asp	Val	Asn
							215					220			
Leu	Trp	Cys	Arg	Gln	Arg	Arg	Val	Lys	Ala	Lys	Ala	Val	Ser	Thr	Gly
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Lys	Lys	Val	Ser	Gly	Ala	Ala	Ala	Gln	Gln	Ala	Val	Ser	Tyr	Pro	Asp
					245					250					255
Asn	Leu	Thr	Tyr	Arg	Asp	Leu	Tyr	Tyr	Phe	Ile	Phe	Ala	Pro	Thr	Leu
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Cys	Tyr	Glu	Leu	Asn	Phe	Pro	Arg	Ser	Pro	Arg	Ile	Arg	Lys	Arg	Phe
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Leu	Leu	Arg	Arg	Val	Leu	Glu	Met	Leu	Phe	Phe	Thr	Gln	Leu	Gln	Val
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Gly	Leu	Ile	Gln	Gln	Trp	Met	Val	Pro	Thr	Ile	His	Asn	Ser	Met	Lys
					310					315					320
Pro	Phe	Lys	Asp	Met	Asp	Tyr	Ser	Arg	Ile	Ile	Glu	Arg	Leu	Leu	Lys
					325					330					335
Leu	Ala	Val	Pro	Asn	His	Leu	Ile	Trp	Leu	Ile	Phe	Phe	Tyr	Trp	Phe
					340					345					350
Phe	His	Ser	Cys	Leu	Asn	Ala	Val	Ala	Glu	Leu	Leu	Gln	Phe	Gly	Asp

	355		360		365	
Arg	Glu Phe Tyr Arg Asp Trp	Trp Asn Ala Glu Ser Val Thr Tyr Phe				
	370	375		380		
Trp	Gln Asn Trp Asn Ile Pro Val His Lys Trp Cys Ile Arg His Phe					
385		390		395		400
Tyr	Lys Pro Met Leu Arg His Gly Ser Ser Lys Trp Val Ala Arg Thr					
	405		410			415
Gly	Val Phe Leu Thr Ser Ala Phe Phe His Glu Tyr Leu Val Ser Val					
	420		425			430
Pro	Leu Arg Met Phe Arg Leu Trp Ala Phe Thr Ala Met Met Ala Gln					
	435		440			445
Val	Pro Leu Ala Trp Ile Val Gly Arg Phe Phe Gln Gly Asn Tyr Gly					
	450		455			460
Asn	Ala Ala Val Trp Val Thr Leu Ile Ile Gly Gln Pro Val Ala Val					
465		470		475		480
Leu	Met Tyr Val His Asp Tyr Tyr Val Leu Asn Tyr Asp Ala Pro Val					
	485		490			495
Gly	Val					

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